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OM nucleic - nucleic search, using sw model

Run on: November 9, 2001, 09:54:43 ; Search time 96.37 Seconds
(without alignments)

10822.295 Million cell updates/sec

Title: US-09-001-737-7
Sequence: 1661
1 GAATTCGGCTCATATGCA.....TGGCGGATTAACCGAATTC 1661

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

N_Geneseq_0601.*
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2: /SIDSI/gcgdata/geneseq/geneseq/NA1981.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1661	100.0	1661	20 AAX86155
2	1052	63.3	1654	20 AAX86153
3	1038.4	62.3	1926	22 AAF25016
4	1033.4	62.3	5365	19 AAV52210
5	942.6	56.7	3635	20 AAX12979
6	704.2	42.4	1647	18 AAT69201
7	704.2	42.4	1647	18 AAT69203
8	654.2	39.4	96109	22 AAF28546
9	590.6	35.6	1665	20 AAX86152
10	589.8	35.5	1647	21 AAA48499
11	589.8	35.5	1647	22 AAC90805

12	589.8	35.5	4524	21 AAA48500
13	568.2	34.2	1662	20 AAX86154
14	552.8	33.3	1635	21 AAX54509
15	551.6	33.2	910715	20 AAX20248
16	550	33.1	2465	12 AAO13135
17	536.8	32.3	1635	21 AAA13000
18	536.8	32.3	1635	21 AA254508
19	536.8	32.3	13423	21 AAB81527
20	536.8	32.3	349960	21 AAF21612
21	528.6	31.8	1838	14 AAB81489
22	528.6	31.8	1838	14 AAO47926
23	528.6	31.8	1838	14 AAO48734
24	528.6	31.8	2223	12 AAO13137
25	527	31.7	1724	19 AAX14495
26	526.6	31.7	1635	21 AA254507
27	512	30.8	1847	22 AAF32452
28	511.2	30.8	1725	22 AAF32453
29	505.8	30.5	1038602	20 AA201425
30	496.6	29.9	2284	16 AAQ90181
31	496.6	29.9	2284	17 AAT45681
32	496.6	29.9	2322	16 AAO75321
33	483.2	29.1	3613	9 AAN80339
34	470	28.3	1017	18 AAV74577
35	464.2	27.9	1737	22 AAF70986
36	461.6	27.8	2847	22 AAF25014
37	460	27.7	1947	22 AAF25019
38	458.6	27.6	1623	22 AAF25002
39	458.6	27.6	1920	22 AAF25012
40	458.6	27.6	4260	9 AAN81768
41	458.6	27.6	4380	9 AAN80222
42	458.6	27.6	4380	19 AAV05708
43	448.8	26.9	1656	20 AA211371
44	448.8	26.8	1647	17 AAT14265
45	444.8	26.8	1569	19 AAV34608

ALIGNMENTS

RESULT 1	
ID AAX86155	Standard: DNA; 1661 BP.
AC AAX86155;	
DT 22-SEP-1999 (first entry)	
DE DNA encoding a Streptococcus pyogenes heat shock protein (Hsp)60-2.	
KW Heat shock protein; Hsp60-2; Immune response; Immunological carrier; cancer control; tumour; sarcoma; cancer; gene therapy; ss.	
OS Streptococcus pyogenes.	
XX WO9935270-A1.	
PN 15-JUL-1999.	
PD 29-DEC-1998; 98MO-CA01203.	
PF 31-DEC-1997; 97US-0001737.	
PR (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.	
XX Mizen L, Wisniewski J;	
PI WPI: 1999-430397/36.	
DR P-PSDB; AAY23904.	
XX New nucleic acid encoding heat shock protein-60 from Streptococcus,	
PT useful in vaccines, as carriers for other immunogens, as anticancer	
PT agents and for diagnosis	
XX	

Escherichia coli g
DNA encoding a Str
Neisseria meningit
Borrelia burgdorfe
Hsp operon. Chlam
Neisseria meningit
Neisseria meningit
N. meningitidis pa
Neisseria meningit
N. meningitidis pa
Hsp60 DNA. Helico
Hsp gene. Helico
Hsp operon. Chlam
H. pylori GHP0 118
Neisseria gonorrhoe
Pseudomonas aerugi
pTCH18B expressio
Complete genome se
Helicobacter pylori
H. pylori heat sho
Heat shock protein
Clone Y3178 insert
Staphylococcus aur
C. glutamicum SRT
Nucleotide sequenc
Nucleotide sequenc
Nucleotide sequenc
Sequence encoding
Sequence of Mycob
Mycobacterium tube
Nucleotide sequenc
Brevibacterium fla
M. vaccae antigen

PS Claim 3; Fig 4A-B; 176bp; English.

XX The present sequence encodes a heat shock protein, designated Hsp60-2.
 CC The protein, its fragments, variants and fusion proteins, are
 CC used to elicit or enhance an immune response against Streptococcus,
 CC and to elicit a similar response to a target antigen fused to the
 CC protein. Unlike other immunological carriers, Hsp60 proteins are not
 CC immunosuppressive so provide an increased response to any conjugated or
 CC fused antigen. Also, where used for cancer control, they lack the side
 CC effects associated with endotoxins. They can also be used to detect
 CC specific antibodies and in treatment or prevention of tumours
 CC (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or
 CC liver). The Hsp60 polynucleotide is used for recombinant production
 CC of the protein, as a source of primers and probes for detecting
 CC streptococci in standard hybridization/amplification assays, and
 CC therapeutically in gene therapy vectors.

CC Sequence 1661 BP; 512 A; 308 C; 407 G; 434 T; 0 other;

Query Match 100.0%; Score 1661; DB 20; Length 1661;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1661; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATGGGCTCATATGCGCAAAAGAAATCAATTTTCACAGATCCGCTCTCCATGG 60
 Db 1 gaatcggctcatatgcaaaaagaaatacaatttcacagatcgcgtctccatgg 60
 OY 61 TGGCGGAGTTGATATGTTAGCAGATACCGTCAAGTAACGCTTGCTTAAAGGCGCA 120
 Db 61 tgcgcgagatgatatgtctagcagataccgtaacgcttgcttctaaaggcgca 120
 OY 121 ATGTGTTCTTGAAGAAAGCTTTTGCTCCCTTAATTAATCAATACGGGTAACCTTG 180
 Db 121 atgtgtcttgaagaaagctttgctcccttaatttaataacgggtaaccttg 180
 OY 181 CTAAAGATGCAATTAGAGATCATTTTGAAGATGGGCAAAATTTGGTGTCTGAAG 240
 Db 181 ctaaaagatcgaattagaagatcatttgaagacatgggcaaaatttgggtctgaag 240
 OY 241 TGGCTTCTTAAACCAATGATATGCTGTGATGGAGCGCTCTGCAAGCTTTTGAAC 300
 Db 241 tggcttcttaaaccaatgatattgctgtgatggagcgctctgcaagcttttgaac 300
 OY 301 AAGCCATTGTTATGAGAGACTAAAAATGTGACAGCAGCTGCTATCAATTTGGATCC 360
 Db 301 aagccattgttatagaagactaaaaatgtgacagcagctgctatcaatttggatcc 360
 OY 361 GTGAGGCAATTGAACAGCAACAGACGCTTTGAAGCCCTGAAAGCCATTGCTCAAC 420
 Db 361 gtgaggcatlgaacacagcaacagcgtttgaagccctgaaagccattgctcaac 420
 OY 421 CTGTATTCGCGAAGAGCTATTGCTCAGGTGCGTGCAGATATCATCGCTTGAAAG 480
 Db 421 ctgtattcgcgaaagactattgctcaggtgcggtgcagatattcatcgcttgaaag 480
 OY 481 TTGGAGATATATCTCAGAAAGCTATGAGCGTGTGGGCAAGCATGGTGTATTACCATG 540
 Db 481 ttggagatatatctcagaaagctatgagcgtgtgggcaagcatgggtgtattaccatg 540
 OY 541 AAGAAATCGAGGATATGGAAGAACTTGAAGTGTGAAGGATGCAATTTGACCGTG 600
 Db 541 aagaaatcgaagatattggaagaaacttgaagtgtgaaggatgcaattttgaccgtg 600
 OY 601 GTTACCTGTCTCAATACATGATGTCACAGACATGAAGAAATGTTGACCTTGAAGAC 660
 Db 601 gttaacctgtctcaatacatgatgtctcacagacatgaagaaatgttgaccttgaagac 660
 OY 661 CATTATCTTAATCAGGATAAAAAGTGTCAACAATCAAGATTTTCCCTACTTG 720
 Db 661 cattatcttaatcaggataaaaagtgtcaacaatcaagattttccctacttg 720
 OY 721 AGGAAGTCTTAAAAACCAACCGTCAATCAATTATTGAGATGATGTGATGTAAG 780

Db 721 aggaagcttcttaaaccaacccgtccattcattctgcagatgctgagtgag 780
 OY 781 CACTTCAACCTGTCTTGAACAAGATGTTGATGTTCAATGTTGTTCTTCAAG 840
 Db 781 cacttcaacctgtcttgaacaagatgttgatgttcaatgttcttcaag 840
 OY 841 CGCAGATTTTGTATGTCGTGTAAGCTTGTGAACATGCTTACTTGTACAGTG 900
 Db 841 cgcagattttgtatgtcgtgtaagcttgtgaacatgcttacttgtacagtg 900
 OY 901 GTACAGTATTTACAGAGATCTAGACTTGAATTAAGATCTCAATGACACCCCTTG 960
 Db 901 gtacagtatttacagagatctagacttgaattaaagatgctacaatgacaccttg 960
 OY 961 GACAGGCTCTTAAGATTACAGTTATGAATGACACATTAATTTGAGTTGAGAA 1020
 Db 961 gacaggctcttaagatttacagttatgaatgacacatthaatttgaagttgagaa 1020
 OY 1021 GTTCAAGGCTTATGCTTACCGGTAATGCTGACTGATTAATCGCATTTAGCAACAATT 1080
 Db 1021 gtccaaggcttattgcttaccggtaattgctgactgatthaattcgcattttagcaacaatt 1080
 OY 1081 CTGACTTGTACCGTGAAGAACTACAGAAACGTTTGCGGAATTAAGTGTGTAGCTG 1140
 Db 1081 ctgacttgtaccgtgaagaaactacagaaacgtttgcggaatttaagtgtgtagctg 1140
 OY 1141 TTATCAAGTATGAGAGCTCAACAGAGACGCTTTAAAGAAATGAACTTCGCTTAGG 1200
 Db 1141 ttatcaagtatgagagctcaacagagacgcttttaagaaatgaaacttcgcttagg 1200
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 Db 1201 atgctctaatgcttaccacgtgacagccgttgaagagatattgctgtgtgtgaacag 1260
 OY 1261 CACTTATACCGTATTGAAAAGTACAGCTTGTGAGCTTGAGGCGGATGATGCTACTG 1320
 Db 1261 cacttataccgctattgaaaagtacagcttgtgagcttgagggcgatgactgactg 1320
 OY 1321 GACGTAAATGTCCTGCTGCTTGAAGAGCCTGTACGTCAAATTTGCTTAAATGCTG 1380
 Db 1321 gacgtaaatgtcctgctgcttgaagagcctgtacgtcaaatgttctaattgctg 1380
 OY 1381 GGTACGAAGGCTCGTATTATGACAAGTTAAGCAAGCCCTGACGAAGACGATTTA 1440
 Db 1381 ggtacgaaggctcgtattatgacaagtttaagcaagccctgacgaagacgattta 1440
 OY 1441 ATGCTGCAACAGTGAAGTGGTGTGATATTAACAGCAATATTGACCTGTCAAG 1500
 Db 1441 atgctgcaacagtggaagtgggtgatatttaacagcaatattgacctgtcaag 1500
 OY 1501 TAACAGATCAGCGCTTCAAAATGACGCTTGTGATGATCTTATTGACAACGAGAG 1560
 Db 1501 taacagatcagcgcttcaaaatgacgcttgtgatgatcttatttgacaacgagag 1560
 OY 1561 CAGTGTGCTTAATTAACCTGGAACCGATACCGACCGCCAGCAATCCAGCAGATATG 1620
 Db 1561 cagtgtgcttaatttaacctggaaacgataccgacccagcaatccagcagatattg 1620
 OY 1621 ATCCAGAAATGATGGGTGGATGGCGGATTAAGCCGGAATTC 1661
 Db 1621 atccagaaatgatgggtggatggcggaatttaagccgggaatttc 1661

RESULT 2
 AAX86153
 ID AAX86153 standard; DNA; 1654 BP.
 XX AAX86153;
 AC
 XX
 DT 22-SEP-1999 (first entry)
 XX
 DE DNA encoding a Streptococcus pneumoniae heat shock protein (Hsp)60-2.

XX Heat shock protein, Hsp60-2; Immune response; Immunological carrier;
 KW cancer control; tumour; sarcoma; cancer; gene therapy; ss.
 XX Streptococcus pneumoniae.
 OS WO9035270-A1.
 XX PN 15-JUL-1999.
 XX 29-DEC-1998; 98KO-CA01203.
 XX PF 31-DEC-1997; 97US-0001737.
 XX PR (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 XX PA Mlizen L, Wisniewski J;
 XX PI WPI: 1999-430397/36.
 XX DR P-PSDB; AAY23902.
 XX PS New nucleic acid encoding heat shock protein-60 from Streptococcus,
 PT useful in vaccines, as carriers for other immunogens, as anticancer
 PT agents and for diagnosis
 XX
 PS Claim 3; Fig 2A-B; 176pp; English.

CC The present sequence encodes a heat shock protein, designated Hsp60-2.
 CC The protein, its fragments, variants and fusion proteins, are
 CC used to elicit or enhance an immune response against Streptococcus,
 CC and to elicit a similar response to a target antigen fused to the
 CC protein. Unlike other immunological carriers, Hsp60 proteins are not
 CC immunosuppressive so provide an increased response to any conjugated or
 CC fused antigen. Also, where used for cancer control, they lack the side
 CC effects associated with endotoxins. They can also be used to detect
 CC specific antibodies and in treatment or prevention of tumours
 CC (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or
 CC liver). The Hsp60 polynucleotide is used for recombinant production
 CC of the protein, as a source of primers and probes for detecting
 CC streptococci in standard hybridization/amplification assays, and
 CC therapeutically in gene therapy vectors.

XX Sequence 1654 BP; 500 A; 326 C; 401 G; 427 T; 0 other;

Query Match 63.38; Score 1052; DB 20; Length 1654;
 Best Local Similarity 77.7%; Pred. No. 1,3e-265;
 Matches 1271; Conservative 0; Mismatches 365; Indels 0; Gaps 0;

QY 1 GAATTCGGCTTCATATGGCAAAAGAAATCAATTTTCAGACAGATGCGGTGCTGCATGG 60
 DB 1 gaattcggcttcataatgcaaaagaataatttcatacgaatgcccgttcgcctatg 60
 QY 61 TCGCGGAGTTGATATGTAGCAGATACCGTAAAGTAAAGCTTGGTCTTAAAGGCGCA 120
 DB 61 tcgcggagttgatattgttagcagataccgttaagtaagtaacttgggacaaaggtcga 120
 QY 121 ATGTGTTCTGAAAAAGCTTTTGGTTCTCCCTTAATTAATGAGGAGGGAATG 180
 DB 121 atgtgttctgaaaaagcttttggttctcccttaatttaattgagggaggtgacatg 180
 QY 181 CTAAAGAGTCGATGATGAGATCAATTTGAAACATGCGGCAAAATTTGCTGGAAG 240
 DB 181 ctaaaagatcgatgagatgagacatttgaataatgaggtgccaattggtatccagaag 240
 QY 241 TGGCTTCTAAACCAATGATGATGCTGATGAGGACACTACTGCAACAGTTTGGAC 300
 DB 241 tggcttctaaaccaatgatgattgctgatgaggaactactgcaacagtttggacc 300
 QY 301 AAGCCATGTTGATGAAAGGACTAAAGATGAGCAGCGGTGATCAATTCATGATG 360
 DB 301 aagccatgttgatgaaaggactaaagatgagcagcggtgatcaattcatgattcc 360

QY 361 GTGAGGCAATTTGAAACAGCAACAGACAGCTGTGAAGCCTTGAAGCCATTGCTCAAC 420
 DB 361 gtgaggcaatttgaaaacagcaacagacagctgtgaagccttgaagccattgctcaac 420
 QY 421 CTGTATCTGGCAGAGGAGTATGCTCAGGTGCTGCAATGATCAACGCTTGAAAG 480
 DB 421 ctgtatctggcagagagatgctcaggtgctgcaatgatcaacgcttgaaag 480
 QY 481 TTGAGAGTATATCTCAGAAAGCTATGAGAGCTGTGCGCAACGATGTGATTAACATG 540
 DB 481 ttgagagtatatctcagaaagctatgagagctgtgcgcaacgatgtgatataacatg 540
 QY 541 AAGAACTCTGAGATGAGTGAAGAACTGAAGTGTGAAGGAGCAATTTGACCGG 600
 DB 541 aagaaactctgagatgagtgaaagaaactgaagtgtgaaggagcaatttgaccgg 600
 QY 601 GTTACCTGTCTCAATACATGCTGCACAGACATGAAAAAAGTTGACAGACTTGAAC 660
 DB 601 gttacctgtctcaatacatgctgcacagacatgaaaaagttgacagacttgaac 660
 QY 661 CATTTATCTTAATCAGGATATAAAGTGTCAACATCAAGACATTTTGCACACTT 720
 DB 661 catttatcttaatcaggatataaagtgtcaacatcaagacatTTTGCACACTT 720
 QY 721 AGGAAGTCTTAAACCAACACCTCCATTACTATTATGACATGATGTGGATGTGAAG 780
 DB 721 aggaagtctttaaaccacacctccattactattatgacatgatgtggatgtgaag 780
 QY 781 CACTTTCACACCTCTGTCTTGAACAGATCTGTGACTTTCATATGTTGCTGTCAAG 840
 DB 781 cactttcacacctctgtcttgaacagatctgtgactttcatatgTTGCTGTCAAG 840
 QY 841 CGCCAGATGTTGGATGACGTCGCAAGCAATGAAAGCAATGCAATGCAATGCAAG 900
 DB 841 cgccagatgttggatgacgtcgcgaagcaatgaaagcaatgcaatgcaatgcaag 900
 QY 901 GTACAGTATTCAGAGACTCTAGACTTGAATTAAGATGCTACATGACAGCCCTTG 960
 DB 901 gtacagtatttcagagactctagacttgaatttaagatgctacatgacagcccttg 960
 QY 961 GACAGCGTCGTAACATTAAGTGAATTAAGATGACAGCAATGATGAAAGGTCAGGA 1020
 DB 961 gacagcgctcgaacatttaagtgaatttaagatgacagcaattgatgaaaggTCAGGA 1020
 QY 1021 GTTCAAGACTTATGCTTACCGTATGCTGATTAATTCGCAATGAGAACACACTT 1080
 DB 1021 gttcaagacttattgcttaccgtattgctgatttaatttcgcaattgagAACACACTT 1080
 QY 1081 CTGACTTGGACCGTGAAGAACTCAAGAAAGCTTTGGGAAATTAAGTGGGTGATG 1140
 DB 1081 ctgacttggaccgtgaagaaactcaagaaagctttgggaaatttaagtggtgatg 1140
 QY 1141 TTATCAAGATGAGAGCTCCACAGAGACAGCTTTAAAGAAATGAATCCGATTGAG 1200
 DB 1141 ttatcaagatgagagctccacagagacagcttttaagaaatgaatccgattgag 1200
 QY 1201 ATGCTCTAATGCTACAGCGGCGGTTGAAGAGATGCTGTGCTGTGAGAAAG 1260
 DB 1201 atgctctaatgctacagcgcggttgaagagatgctgtgctgtgagaaag 1260
 QY 1261 CACTTATTAACGTTATGAAAAAGTAAAGTAAAGCTTTGAGGCGCATGATGCTACTG 1320
 DB 1261 cacttattaacgtttatgaaaaagttaagtaagctttgaggcgcatgatgctactg 1320
 QY 1321 GACGTAACTATGCTGCTTCTGCTGCTGAGAGAGCTGTACGTAATTTGTTAAATGCTG 1380
 DB 1321 gacgtaaactatgctgcttctgctgctgagagagctgtacgtaattttgTTAAATGCTG 1380
 QY 1381 GGTACAGAGGCTCCGATGATTAAGCAAGTGAAGAAACACCTGACAGAAAGATTTA 1440
 DB 1381 ggtacagaggctccgatgatattaagcaagtgaagaaacacctgacagaaagattTA 1440
 QY 1441 ATGCTGACAGAGGTGAGTGGGTGATGATTAAGCAAGAAATCATGACCTGTCAAG 1500

Db 1441 acgcagcaactgagcagtgagtgtaacatgcatgtaacagatcatcattgacagtaag 1500
 Oy 1501 TAACAGCATCAGCGCTTCAAAATGCAGCTTGTAGCTGTCTTATTTTGACACAGAAG 1560
 Db 1501 ttagtgcgttcagccctacaaatcagcattcttgagccattgatttgacaacagaag 1560
 Oy 1561 CAGTTGTTGCTAATTAACCTGACACGCTACGCCAGCCAGCAATGCCAGCAGTATGG 1620
 Db 1561 cagtcgtcagccataaacacagacagtagcaccagctccagcaatgagatccaatgta 1620
 Oy 1621 ATCCAGAAATGATGGG 1636
 Db 1621 tgggtggaatggcg 1636
 RESULT 3
 AAF25036 standard; DNA; 1926 BP.
 ID AAF25036 standard; DNA; 1926 BP.
 AC AAF25036;
 DT 30-APR-2001 (first entry)
 DE Nucleotide sequence of Hsp65-E7 fusion protein.
 XX
 KW Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell;
 KW Lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
 KW E7 protein; ss.
 XX
 OS Synthetic.
 OS Streptococcus pneumoniae.
 OS Human papillomavirus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1926
 FT /tag_2
 FT /product_ "Hsp65-E7 fusion protein"
 PN MO200104344-AZ.
 PD 18-JAN-2001.
 PF 10-JUL-2000; 2000MO-US18828.
 PR 08-JUL-1999; 99US-0143757.
 PA (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 PI Siegel M, Chu NR, Mizen LA;
 DR WPI: 2001-138361/14.
 DR P-PSDB: AAB31619.
 PT Screening for compounds that stimulate Th1-like responses in CD4+ T
 PT lymphocyte cells.
 PS Example 15; Fig 15A-B; 88pp; English.
 XX
 CC The present sequence encodes a fusion protein comprising a
 CC Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HPV16 E7
 CC protein. The fusion protein is used in the method of the invention. The
 CC specification describes a method of determining whether a compound
 CC stimulates a Th1-like response. Th1 cells are a subset of CD4+
 CC T lymphocyte cells. The method comprises contacting naive lymphocytes
 CC in vitro with a fusion protein comprising at least a fragment of Hsp,
 CC and then detecting the Th1-like response exhibited by the cell sample.
 CC The proteins which may be used in the method of the invention are Hsp65,
 CC Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify
 CC compounds that stimulate Th1-like responses in response to microbial
 CC pathogens.
 SO Sequence 1926 BP; 585 A; 382 C; 464 G; 495 T; 0 other;

Query Match 62.5%; Score 1038.4; DB 22; Length 1926;
 Best Local Similarity 77.5%; Pred. No. 5.2e-262;
 Matches 1238; Conservative 0; Mismatches 366; Indels 0; Gaps 0;
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 Db 1 atggcaaaagaatcaaatcttccatccagatgcgccttcagatgctcgtggtgat 60
 Oy 75 ATGTAGACAGATACCGTCACAAAGTACGCTTGCTCTAAAGGGCGCAATGTCTTGA 134
 Db 61 atccttcagatcagcttgaagtaacttgggccaagagtcgcaatgcttcttgaa 120
 Oy 135 AAAGCTTTGGTTCCTTCAATTAATTAAGAGGAGGTAACCATTTGAAGAGATGAA 194
 Db 121 aagcattcgttcacccttgattaccatagcagtggtgactattgccaagaatgaa 180
 Oy 195 TTAGAAGATCAATTTGAAACATGGAGCAAAATTTGCTGTGAAGTGGCTTAAACC 254
 Db 181 ttagaagaccatttgaataataatcgggccaacttggatcagaagtgcctcaaaacc 240
 Oy 255 AATGATTTGCTGTGATGGAGCACTACTGCAACAGTTTGTACACAGCCATTGTTCAT 314
 Db 241 aatgatattcgaagtgtagtaactacaactgcaactgtttgacccaagcattcgt 300
 Oy 315 GAAGACATAAAATGTGACAGCAGGTGCTAATTCATTTGATTCCTGACGATTTGAA 374
 Db 301 gaagaaatcaaaaatgacacagcagcagtgcaaatcccaatcgatctgctggatgaa 360
 Oy 375 ACAGCAACAGCAACAGCTGTGTAAGCTTTGAAGCCATTGCTCAACCTGATTCGCAAG 434
 Db 361 acagcagtgctgcgacagtgtagaacttgaataaaacagctcaatcccttgcaataaa 420
 Oy 435 GAAGCTATTGCTCAGTGCCTGCTGATATCATCATGCTGTGAAAGTGGAGGTATATC 494
 Db 421 gaagctatcgtctcaagtgtagcagcgtatcttcttcttgaataaagtgtgtgataac 480
 Oy 495 TCAGAAAGCTATGAGCGCTGTGGCAACGATGCTGATTTACCATCGAAGATTCGAGGT 554
 Db 481 tcgaagaagaaatgaaaagtgtgcaaaagcgggtgcatcacatcagaagatcagtg 540
 Oy 555 ATGGAACAGAACTTGAAGTGTGTTGAAGCAATTTGACCGTGTACGTCTCAAA 614
 Db 541 atggaacagagcttgagtcgtagaagaatgagcgttgcgtgtaccccttcaacg 600
 Oy 615 TACATGCTCACAGCAATGAAAAATGTTGCAACCTTTGAACCCATTATCTTAATC 674
 Db 601 tacatgctcagacatgaaaaatggttgcaacctttgaaaaaccattatcttaac 660
 Oy 675 ACGGATAAAAAGTGTCAACATCCAAAGCATTTTGCACACTACTTGAAGAAGTTCTTAA 734
 Db 661 acggaagaagaatctccatccatccagaatcttgcaccttggaaagcattccaa 720
 Oy 735 ACCAAGCTCATTTACTACATTTATTCAGATGATGATGATGATGATGATGATGATGAT 794
 Db 721 agcaatcgtccactcttgatcattcgtgagatcgagtcgagtcgagtcgagtcgagtc 780
 Oy 795 GTCTTGAACAAGATTGCTGACTTCAATGTGTTGCTGTCAAAAGCCCGAGATTGTGT 854
 Db 781 gtttgaacaagaatcttgagaaacctcaacgtagaagcagcagcagcagcagcagcagc 840
 Oy 855 GATGCTGTAAAGCTATGCTGTAAGCAATTTGATTTGCAAGGTGATGATGATGATGAT 914
 Db 841 gacgtgcgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 900
 Oy 915 GAGGATTCAGACTTAAATTAAGATGCTACATGACAGCCCTTGACAGCGCTGTAG 974
 Db 901 gaagaccttgcttcttgatgaaagatgagcaactgagcagcagcagcagcagcagcagc 960
 Oy 975 ATTACAGTATTAAGATGACAGATTTGTTGAAGTTGATGAGTTGATGAGTTGATGAGTT 1034
 Db 961 gtgacgttgacaagaatgacagcagcagcagcagcagcagcagcagcagcagcagcagc 1020

[illegible][illegible]

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Db 757 ctctgaagcaatgtaaaagttgcaaaagacggtgcatcaccatcgaagagtcacgtg 816
OY 554 TATGAAACAGAACTGGAAGTGTGGAAGCATCATTTTGACCGTGTCTCA 613
Db 817 tatgaaacagagcttgaagtcgtagaagaaatgcaattgaccgtgtacccctcaca 876
OY 614 ATACATGTCACAGACATGAAATAATGTTGACGCTTGAAACCCATTATCTTAAT 673
Db 877 gtacatggtacagataagcaaaatggtgctgacctgtaaatccgtacatttggat 936
OY 674 CACGGATAAAAGTGTCAACATCAAGACATTTTGCCACTACTTGAGGAAGTTCTTA 733
Db 937 tacagacaaagaaatctccaaataccagaatctctgcaactcttggaagaacatctcca 966
OY 734 AACCAACCGTCTTACTCATTTATTCAGATGTGATGTGATGAGCACTTCCACCT 793
Db 997 aagcaatctgcccactcttgatctatgctgagatggtggtgaggtctctcacaactc 1056
OY 794 TGTCTTGACAAAGATTCGTGACTTCAATGTGCTGCTGCTGCTGCTGCTGCTGCT 853
Db 1057 tgtttgaaacaaagattcgtggaaccttcaacgtagtagagcaagcaacctgcttctg 1116
OY 854 TGATCGTCCGTAAGCATGCTTGAAGACATTCCTTTCAGACAGGTGCTACAGTATAC 913
Db 1117 tgaacgctgcgaagacatgcttgaagatacgcacatcttaacagcggaacagatcac 1176
OY 914 AGAGATCTAGACTTGAATTAAGATGCTACATGACAGCCCTTGACAGGTGCTGCTAA 973
Db 1177 agaagaccttgcttctgagttgaaagatgcaacatctgacatctctgtaagaagagag 1236
OY 974 GATTACAGTTGATTAAGATACACAGTATTTGTAAGTTTGAAGACTTGAAGACTTAT 1033
Db 1237 agtgaacgctgcaaaagacagacgltacttgaaaggtgcaagaaatccctgaagagat 1296
OY 1034 TGTAAACGCTATTCATGATTAATTCGCAATTGAAACAAACACTTCTGACTTGCACG 1093
Db 1297 ctccacgctgttcggtgltacaaagctcacaactcgaactacactctgatttgaacg 1356
OY 1094 TGAATAATACAAAGATGCTGGAATTAAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1153
Db 1357 tgaataatgcaaaagacgctgcaaaatgctcaaggtggtgcaaggtctcttcaagat 1416
OY 1154 AGCTCCACAGACAGACGCTTTAAAGAAATGAATCTCGCATTCAGATGCTGCTAAATGC 1213
Db 1417 agcgcgaactgaactgagttgaaagaaatgaactccgcatctgaagatgcctcacaagc 1476
OY 1214 TACACGTGACGCGCTTGAAGAAGTATCGTGTGCTGCTGCTGCTGCTGCTGCTGCT 1273
Db 1477 tactcgtgagcgtgtgaaagaggtatctgtcaggtggtgaaagacatctcgaatgt 1536
OY 1274 TATGAAAAATAGACGCTCTTGACCTTGAGGCGCATGATCTACTGAGCTAATCTGT 1333
Db 1537 gattcgaactgtctcactccttgaaattgacagaaatgaagcaacagaaagtaattgt 1596
OY 1334 GCTTGCTGCTCTAGAAAGACGCTGATCAATTCCTTAATCTGCTGCTGCTGCTGCTGCT 1393
Db 1597 tctcgcgtcttggaagaaacgctgtcgaactgtcacaatgcaagatgtaagaaatc 1656
OY 1394 CGTATGTTTTCACAAGTTGAAAACAGCCCTCAGAGAACAGATTTAATCTGCAACAG 1453
Db 1657 tatcgtatcgtatcgttctgaaataatgctgagttagattcaacagcaactctg 1716
OY 1454 TGAAGTGGTGTGATGATTAAGACAGAAATCATTCACCTCTCAAGATTAACAGATCAC 1513
Db 1717 cgaatgggttaacatgattgataagatctatgacatctcagtaagttgctgcttgcagc 1776
OY 1514 GCTTCAAAATGACGCTCTGATGCTGCTTATTTTGAACAAGAGAGTGTGCTTA 1573
Db 1777 cctacaaatgcaatcctgtaagcagctgtcttgcaacagaaagcagtcgtgcaaa 1836
OY 1574 TAACTTAACACAGCTACGCGACCGCACAGATGCGACAGTATGATTCAGAGATAT 1633

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Db 1837 taaacgaagaccagtaagcccaagctccagcaatgataccaagcatgagggcggatgat 1896
OY 1634 G 1634
Db 1897 g 1897

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RESULT

5

AA12979
ID AA12979 standard; DNA; 3625 BP.

AA12979;

19-MAR-1999 (first entry)

Enterococcus faecalis genome contig SRQ ID NO:42.

KW Enterococcus faecalis; contig; detection; Enterococcal infection;
KM vaccine; attenuation; computer readable medium; ds.

OS Enterococcus faecalis.

PN WO980555-A2.

PD 12-NOV-1998.

PF 04-MAY-1998; 98NO-US08985.

PR 14-NOV-1997; 97US-0066009.

PR 06-MAY-1997; 97US-0044031.

PR 16-MAY-1997; 97US-0046555.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Barash SC, Dillon PJ, Kunsch CA.

DR WPI: 1999-045171/04.

PT New isolated Enterococcus faecalis polynucleotides and polypeptides
PT - used to develop products for the detection of Enterococcus
PT use in vaccines for prevention or attenuation of Enterococcus
PT infection.

PS Claim 1; Page 414-416; 2084pp; English.

CC A computer readable medium has been developed which has recorded on it
CC 982 nucleotide sequences isolated from the Enterococcus faecalis genome.
CC AA12938 to AA13919 represent these nucleotide sequences which are
CC primary nucleotide sequences, also known as contigs. The computer-based
CC system can identify fragments of the Enterococcus faecalis genome with
CC commercial importance. The products can be used to detect the presence
CC of Enterococcus faecalis in samples. They can also be used for
CC diagnosing Enterococcal infection in an animal and monitoring
CC progression of disease, and for identifying agents which can be used to
CC modulate the growth or pathogenicity of Enterococcus faecalis, or
CC another related organism, in vivo or in vitro. In particular the
CC polypeptides encoded by the Enterococcus faecalis nucleotide sequences
CC can be used in vaccines to prevent or attenuate an Enterococcal
CC infection.

SO Sequence 3625 BP; 1335 A; 542 C; 750 G; 993 T; 5 other:

Query Match 56.7%; Score 942.6; DB 20; Length 3625;
Best Local Similarity 74.2%; Pred. No. 7.8e-237;
Matches 1191; Conservative 0; Mismatches 415; Indels 0; Gaps 0;

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OY 15 ATGGCAAAAGAAATCAATTTTCACAGATGCGGCTGCTCCATGCTGCGCGAGTGTAT 74
Db 364 atgcaaaagaaatcaatcttgcagaagatgcaagtcagcaatgtctacgagatgat 423
OY 75 ATGTTGCAAGATACCGTCAAGATTAAGCTGTGCTTAAGGCGCAATTTTCTTGA 134

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Db 424 gattatagcagatlacagtgaaagtgacattagagccctaaaggtcgttaacgtgttttagaa 483
 QY 135 AAAGCTTTTGGTTTCCCTTAATTACTAATGACGGGGTACCACTTGTAAAGATCGAA 194
 Db 484 aatcatttggttcacattactactaagcgtggaatacaattgcttaaggaattgaa 543
 QY 195 TTAGAGATCATTTTGAACATGAGGACCAAAATTTGTTGTTGAAGTGGCTTAAAC 254
 Db 544 ttggaaagtacattttagaacaacatggcgcaaaattagttcagaagttgtcttcaaaag 603
 QY 255 AATGATATGCTGTGTCATGTCGACGACTACTGCAACAGTTTGACACAAAGCAATTTTCAT 314
 Db 604 aatgatacttctgtgacggaacaacaacagcactgtttgcacaagacattgttcgt 663
 QY 315 GAAGACTATAAATGTGACAGCAGGTGCTAATCCAAATGTTATCTCGCAGGCAATGAA 374
 Db 664 gaagccttaaaaaacgtaacctgtgagcacaacccattaggtatcgtcgttgattgaa 723
 QY 375 ACAGCAACAGACAGCTGTGTAAGCCTTGAAGCCTTGAAGCCTGTAATCTGCAAG 434
 Db 724 ttggacaacaacaacagcagtagaagaattacacaatatlcatcgttagttgattcaaa 783
 QY 435 GAAGCTATTTGCTGAGTGCCTGCTGAGTATCATCGCTCTGAAAAGTTGAGATATATC 494
 Db 784 gaagcatttgacaaagcgtgtgttcatcaggttctgaaaaagtcgccaataatt 843
 QY 495 TCAGAACGCTATGAGCGTGTGGGCAACGATGCTGATTAACATCGAAGAAATCTCGAGT 554
 Db 844 gcgcctgcaaatgtgaaaaagtcgtcaacgacgycatattccacttgaatcgaatcaaaagg 903
 QY 555 ATGAAACAGAACTTGAAGTGTGTTGAAGGCAATGCAATTTGACCGTGTACTCTCAA 614
 Db 904 atcgaaacagattagctgtgtgagaaagcattcgacgctgtattatctatcctaa 963
 QY 615 TACATGCTCAGACAGTAAAAATGTTGCGACGCTTGAACCACTTATCTAATATC 674
 Db 964 taactgttactcgaacaaagataaatgtgaagctgtcttagaataaccatactaatc 1023
 QY 675 ACGGATTAATAAAGTGTCAAAACATCCAGACATTTTGCACACTTGAAGAATCTTAA 734
 Db 1024 accgacaaaaaaatcctcaaatctcaagatcttacccttattagaaacaattctaca 1083
 QY 735 ACCAAGCTCCATTACTTATTCAGATGATGATGATGATGATGATGATGATGATGATGAT 794
 Db 1084 caaagccgctcactactatgtattatcgtgagatgtctgtgagaaagcctcaacaacat 1143
 QY 795 GTTTGAACAAGATTCGTGTACTTCAATGTGTGTTGCTGTCAAGCGCAGATTTGGT 854
 Db 1144 gtattgaaacaataccgtgtacattatgtgtcgcagaaagcgcagagattggt 1203
 QY 855 GATGCTGTAAAGCTATGCTGTAAGACATGCTATCTGACAGGTTGATACAGTATTA 914
 Db 1204 gacgcgcgcaaaagcgtatgtcgaagatattgtctattcaacagtggtacagaatcact 1263
 QY 915 GAGATCTAGACTGTGAATTAATAAGTGTACAAAGACAGCCCTTGACAGGCTGTAA 974
 Db 1264 gacgacttaggttagagtttaaaagacacaactatctgaataacttagaagcgtacaa 1323
 QY 975 ATTACAGTGTAAAGATGACAGATATTTGTTGAAGTTGAGAAATTTGAGAGCTATT 1034
 Db 1324 gtatgttcgcaaaagataaacaacaaatgtcgaagtggtgttcaaaagagtcatt 1383
 QY 1035 GCTAACGCTATTCAGCTGATTAATCGCAATTAAGAACACACACTTGTGCTTTGACCT 1094
 Db 1384 gatgcgcgctcacttaataaaaaacaaacaaacgcaaaacgctgttctgtcgt 1443
 QY 1095 GAAAACTACAGAAAGCTTTGGCAATTTAGCTGTGTGTGTGTGTGTGTATTAACAAGTGA 1154
 Db 1444 gaaaaactacaagaacgcttagctaaattagctgtgtgtgtgtgtgtgtgtgtgtgtgt 1503
 QY 1155 GCTCCACAGAGACGCTTAAAGAAATGAAACTGCAATGAGTGTGCTGCTAAATGCT 1214
 Db 1504 gctgcacacgaacgaattaaaaagaattcaaatcgaattggaagatgcattcaacgca 1563

QY 1215 ACACGTGACGCCGTTGAAGAAGTATCGTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1274
 Db 1564 aacgtgcgcgttagaagaagcagcagttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1623
 QY 1275 ATTGAATAAGTACAGCTCTTGTGAGTGGGCGATGATGCTACTGACGTAACATGTTG 1334
 Db 1624 attgttaagtcgt 1683
 QY 1335 CTTCGCTGTAGAAAGCCCTGTACGTCATATGCTTTAAATGCTGGGTACGAAGCTCC 1394
 Db 1684 gtctgtattagaagaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 1743
 QY 1395 GTAGTTATGACAATGTAAGAAACACGCCCTGACGACAGATTAATGCTGTGACAGAT 1454
 Db 1744 gtgattgttgcaaacataaaatgttgaactaagttatcgattcgaattcgaactaagtc 1803
 QY 1455 GATGAGTGTGATGATTAATAACAGAAATCATTTGACCTGTCAAAAGTACAGATCAG 1514
 Db 1804 gaattggttaaacatgltgaaagcgttatgttgaccacaacaaagtaactcgttctcc 1863
 QY 1515 CTTCATAATGACGCTTCTGTAGCTAGCTTATTTTGTGACACAGACAGATGTTGCTAAT 1574
 Db 1864 ttcaaaatgagcttctgtgcagcttattatlaaacaactgaagcagttgtgtgagac 1923
 QY 1575 AAACCTGACACGCTACGCCACGCGCACCAATGCCACAGTATG 1620
 Db 1924 aaaccgaacagctgac 1969

RESULT 6

AAT69201
 ID AAT69201 standard; DNA; 1647 BP.
 XX
 AC AAT69201:
 DT 20-AUG-1997 (first entry)
 XX
 DE Lawsonia intracellularis GROEL DNA.
 XX
 KW Intestinal disease; porcine proliferative enteropathy; vaccine;
 GROEL; heat shock protein; ss.
 XX
 OS Lawsonia intracellularis.
 XX
 PN WO9720050-A1.
 XX
 PD 05-JUN-1997.
 XX
 PF 29-NOV-1996; 96MO-AU00767.
 XX
 PR 30-NOV-1995; 95AU-0006911.
 PR 30-NOV-1995; 95AU-0006910.
 XX
 PA (DARA-) DARATECH PTY LTD.
 PA (PIGR-) PIG RES & DEV CORP.
 XX
 PI Hasse D, Panacelo M;
 XX
 DR WPI: 1997-310605/28.
 DR P-PSDB: AAM1678.
 XX
 PT Vaccine for treating or preventing Lawsonia intracellularis.
 PT Infection - especially in pigs, containing non-pathogenic form of
 PT bacterium or its components
 XX
 PS Claim 12: Page 38-42; 94pp; English.
 XX
 CC A DNA molecule (AAT69201) codes for the GROEL heat shock protein
 CC (AAM1678) of Lawsonia intracellularis, the causative agent of porcine
 CC proliferative enteropathy (PPE). A genomic library was prepd. from
 CC L. intracellularis PPE lesion isolates and screened with rabbit
 CC anti-L. intracellularis antiserum. Phagemid DNA was isolated from

OY	19	CAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCATGGTGCGCGGAGTTATATGT	78
Db	8	ctaaagaatctctctttgtagtctaaagccggtgaaacaattccaaagcggtgataaac	67
OY	79	TAGCAGATACCGTCAAGTAAAGTAAAGCTTGCTGCTTAAAGGGGCATATTGTTCTTGAAAGA	138
Db	68	ttgcaaatgctgtttaagtaaaccttggaaacttaagccgtaagtctgtattgtaaaagt	127
OY	139	CTTTTGCTTCCTCCCTTAATTACTAATGACGGGGTAACACTTTCCTTAAGAGATGAATTAG	196
Db	128	ctttgtgtcccaactatcaataaagaatggtgatactgtgcgaagaatattgaacttg	187
OY	199	AGATCATTTTGAAGAACATGGAGGACGAAATTTGGTGTCTGAATGGCTTTTAAACCAATG	258
Db	188	aagataagtttgaagaataatggtgcgtcaaatggtttaagaagtagctcccaaacatg	247
OY	259	ATTATTCGTCGAGTGGAGGACGACTACTGCAACAGCTTTTGACCAAGGCATCTGTTATGAG	318
Db	248	atatgtcgtgtagtgaactcaacaagaagctcttgcacaagaacttattgtgtaag	307
OY	319	GACTAAAAAATGTGATACGACGAGTGTCTAATCCATTTGTTACCGTCGAGCATTGAACAG	378
Db	308	ggttaaacctgtgaacgcgtgcgaatcccttgcacattaaagcgtgataagataag	367
OY	379	CAACAGCAACAGCTGTTGAAGCCTTGAAGCCATTGCTCAACGTAATTCGCAAGAG	438
Db	368	cgtgtgttcgttacttaagaagataagcacaatttcaaacgctacacgtgcgaacaaag	427
OY	439	CTATTGCTCAAGTTCGCTGGAGATATCATCAGCCTCTA---AAAGTTGGAGAGTATATCT	495
Db	428	aaatagctccaagtttgaaccattctctgcaacctcgtatacaacaatagtaatatcatag	487
OY	496	CAGAGCTATGAGAGCTGTGGGCAACATGCTGTATTCATCCATGAAGAAATTCGAGGA	555
Db	488	cgtgaagctgaagtctaaagtctggaagaagtggttatacaagttgtaagaagataaggtc	547
OY	556	TGGAACAGAACTTGAAGTGGTGAAGGCAATGCAATTTGACCGTGTATTCGCTGTCAAT	615
Db	548	ttgaaactcaactaagatctgtgttgaagaatgaagtcttgcacgtgcctacccctccat	607
OY	616	ACATGTGTACAGCATGTAAAAAATGGTTCGAGACCTGGAAAGCCATTATCTAATCA	675
Db	608	actttgtacttaactcctggaagaatggtcttgtgaactctgtaaacacctataactcttgta	667
OY	676	CCGATAAAAAAGTGTAAACATCCAAAGCAATTTTCCACTACTTGAGGAAGTTCTTAAA	735
Db	668	atggaataaaagaattactcagcgtgaagaagacactctacccaattttagaacaagctgtctaa	727
OY	736	CCAAACCGTCATTACTATTTATGCAGATGATGTGATGAGTGAAGCACTTCCAAACCTTG	795
Db	728	ttaaaccgttccaacctctatactgtctgaagaagcttagaagtggaaggaacttgaacacttg	787
OY	796	TCTTGAACAAGATTCTGTGTACTTCTTGAAGTGTGTGCTGCAAGAGCGCAGGATTTGGG	855
Db	788	tagtcaatatgaagcccggtgagcactccaagttgttagccgttaaaagctcccggtcttggg	847
OY	856	ATCGTCTAAAGCTATGCTGTAAAGACTTGTGTAATTTGACAGAGGTACAGTGTACAG	915

D	b	848	aagcgcglaagctatgcttgaagatatgtctatcccttccttcgtagggagaagcaataattcg	907
O	y	916	AGGATCTAAGACCTTGTAATTAAAAGATGCTCAATGCACCCTTGGACAGCGTCGTAGA	975
D	b	908	aaggctcggtcataaaagctctgaaaattgaagcttgctctctcttttggaaacgctaacytg	967
O	y	976	TTACAGTTGATAAGATGACACAGTAATTTGTGAAGTCAGAAAGTTCCAGAGCTAATG	1035
D	b	968	tagtatcttgcacaagaanaactactactactcgltgtagtgcgtcggtaaatcgaagatatta	1027
O	y	1036	CTAACCGTATTGCGATGATTAATGCGAATTTACAACCAACAACCTTGCATTTGACCGTG	1095
D	b	1028	aagctcgagttaaacaactatcgtagcaaaatcggaaagaacgctcagattatgatcgtag	1087
O	y	1096	AAAACTACACAAAGCTTTGGCGAAATTTAGCTGTGTGTAGCTGTTATCAAGTAGAG	1155
D	b	1088	aaaaactccaagaagctctctgcaaaactbtgtgtgtagctagctgtatccatggttag	1147
O	y	1156	CTCCACAGACGACAGCTTTAAAGAAATGAAACTTGCGATTGAGAGATGCTTAATGCTA	1215
D	b	1148	ctgtactgaacctgaagtgaagaagaagaagatcogttagaagatgctcctaattgcaa	1207
O	y	1216	CAGGTGACGCCCTTGAGAAAGGTATCGTTCTGTGTGTGTGCAACGACCTATTACGGTTA	1275
D	b	1208	caagagctcggtctgaaaagaagatttgtcccgtgtgtgtgtagctctctgtccgtcca	1267
O	y	1276	TTGAAAAAGTAGCACGCTTGTAGCTTGAGGGCGATGATG--CTACTGCAGCTAACATTG	1332
D	b	1268	ttaagtlccttgatgatatataaacctgcgtgatalgatlgaacttgcgtgaacttaalca	1327
O	y	1333	TGCTGTGCTCCTGTACAAAGCGCTGTGACGCAAAATGCTTTAAATGCGGTACGAAGCT	1392
D	b	1328	tcgctgtctctcttgaagaagcctttaagcttaagctcgaactgcgcaaaagctcgctagaagct	1387
O	y	1393	CCGTAGTTATTACAAAGTTGAAAAACAGCCCTGCAGAACGATTTAATGCTGCACAC	1452
D	b	1388	cctctctctgtagaaaagctctgtgaaccaaaagaatgagcttgygattgaattcgtcatcag	1447
O	y	1453	GTAGTGCGGTGATATGATTAAAACAGAAATCATGACCTGTCAAAAGTACACATCAG	1512
D	b	1448	gagaataatgaagaccttattaaagctcggtcatattgatccataaaagttacaagctatg	1507
O	y	1513	CGCTGAAAAATGCACGCTCTGTAGCTAGTCTAATTTGACAAACGAAGAGTTGTGCTA	1572
D	b	1508	cattacaataatgcagcatcagtcagctcccttcaactcaacacagaatcgcgtatttgctg	1567
O	y	1573	ATTAACCTGCAACC 1585	
D	b	1568	aaaaaccagaacc 1580	
<hr/>				
R	E	S	RESULT	7
P	N	I	AAT69203	
R	E	S	AAT69203 standard; DNA: 4972 BP.	
P	N	I	AAT69203;	
R	E	S	20-AUG-1997 (first entry)	
P	N	I	Lawsonia intracellularis vaccine candidate DNA.	
R	E	S	Intestinal disease; porcine proliferative enteropathy; vaccine: ss.	
P	N	I	Lawsonia intracellularis.	
R	E	S	WO9720050-A1.	
P	N	I	30-NOV-1995; 95AU-0006911.	
R	E	S	30-NOV-1995; 95AU-0006910.	
P	N	I	29-NOV-1996; 96MO-AU00767.	

[illegible][illegible]

[illegible]

Db	49636	aaagcgcgtacgcgcgcgtctgttgaaagaatcgcgtglatctcgcgaacccgtcattagacat	49635
Qy	435	GAAGCTATTGCTCAGCTCGCTCGCAGNATATATACCTCT--TGAAAAAGTTGGAGAGTAT	491
Db	49656	aaagcatttcgcaccaagtttggctccaattctcagaagaacctcaagatcctcatttggtagctt	49755
Qy	492	ATCTCAGAAAGCTATGGAACCGCTGTGGCAACGATGGTGTGATATGCATCCAAATATTCGA	551
Db	49756	atctccaagcgaattggaataacagcttggcacaacaagcgttatccacagttcagaaggggttca	49811
Qy	552	GGATATGGAACAGAACTTGAAAGGTGTGAAGGCATGCATTTGACCTGGTACCCTGCT	611
Db	49816	ggtttcgaaagatgcgccttgtaagtaagcttcggggcagaagcatttgcacgvtgcataatcagc	49875
Qy	612	CAATACATGCTCAGACCAATGAAAAATGTTGCGACACTTGAAAAACCATTTATCTTA	671
Db	49876	ccttacttgcacaataacaagaacgacttgacttggtaatttgaatccatcttattctt	49933
Qy	672	ATACAGATAAAAAAGTGAACATCCAAACATTCGAACATTTGGCACTATTGGAGAGTTCTT	731
Db	49936	ttgctgcataaaaaaatctcaatattctgtgagatttgcgtcactacttgaaaaaagtatg	49995
Qy	732	AAACACACCGCTCATTAATCATATTTGCAAGATGATGATGATGATGATGATGATGATGATG	791
Db	49996	caaaccaacgcgcgcgcgcatttaacattcgttgagatatttgaataatgaagcattgcacaa	50055
Qy	792	CTTGCTTGAAACAAGATTCTGTGTACTTTCATATGTGTTCTGTCTGCAAGCCCGAGATT	851
Db	50056	ttgattgttcaatacttctgcgttcggtatataaaactctgcgttcttaaaagccaggttt	50115
Qy	852	GGTATCGTCGTAAAGCTATGCTGTAAGCAATTCCTCTCTGTGACAGGTGATGATGAT	911
Db	50116	ggtgatccgcgttaaaagcscatgcgtctcaagacttgcatttcaacacggcgtgcgtgttacc	50175
Qy	912	ACAGAGATCTAGACTGTGAATTAAGAATGCTCAATGACACCCCTTGACAGGCTGCT	971
Db	50176	tcgaagaagcgggacttaagccttcgaagccttcgaatttcgaatttgggtactgcacaa	50235
Qy	972	AAGATTACAGTTGATTAAGATATAGCACACGATTAATTTTAAAGTTCAGGAAGTTCGAAGCT	1031
Db	50236	aaagtaaacatttggtaaaagaacacgcgtcattcttgatvtgcagtcgagtcgataaagccagc	50295
Qy	1032	ATTGCACTCGTATGACACTGATTAATATCGCAATTAACAACAACAACCTTCGACTTTGAC	1091
Db	50296	attggagcgcgctgtaagagccaattcgttcgtcaagtttgaaagaatcaacttcgcataagcc	50355
Qy	1092	CCTGAAAAACTACAAAGACGTTTGCCGAATTAAGCTGTGGTGTGATGCTTTATCAAGTA	1151
Db	50356	aaagaataaaccttcaagaagcgttgcgcaaaactatcaagcggcgttgcgcattcaaaagtgc	50415
Qy	1152	GGAGCTCCACAGACGACCTTTAAACAAATGAACTTCGATTAAGAGATGCTCTAAAT	1211
Db	50416	ggttcgysaaactgaactcgaatcgaatgaagaagaaaaagcgcgtgtagcagatgacttaac	50475
Qy	1212	GCTACAGCTGACGCGTGTAAAGATGATGCTGTCGTGGTGGTGAACAGCACTTATTACG	1271
Db	50476	gctaccgcgtgcgcgttcgaagaaggcgttcggtccgcggcggcggcgttgcactcttgcgct	50535
Qy	1272	GTTATTGAAAAAGTACGACGCTTTGACCTTTGAGGCGGATGATGCTACTGACGCTTAACAT	1331
Db	50536	gcttattatctgcattaaagcagccttaaaagtgataatgaagaacaaataatgcagcatcaat	50595
Qy	1332	GTGCT--TGCTCTCTTAAACAGACGCTGTACGTCGAATTTGCTTTAAATGCGGTGTCGA	1388
Db	50596	atctcaacgcgttcgtagtgaagcacacccttcgcacaaatcgtcagtaacagcagtgtagag	50655
Qy	1389	GGCTCCGAGCTATTATACAAAGTTGAAAAACAGCCCTCGACAGAACAGATTTAATGCTGCA	1448
Db	50656	gcttcctgaattctcattgaagtttaaaaaatggctcgcgtgaactcaggttctaattgtctga	50715
Qy	1449	ACAGGTAGGTGGTGTGATATGATTAACACAGAAATCATTTGACCTGTCCAAGTAAACGA	1508
Db	50716	tcaggtgaagatgtgcgaattcttggaaattgggtatttgcatttgccttcgcgaagtaaacccgt	50775

QY 1509 TCAGCGCTTCAAAATGACGCTTCGTAGTACTGTTATTTTGACAGACAGACGACTTGT 1568
 DB 50776 tcagcacttgaacaacgctcctcgcaggttctgtatgttgcacactgaagtatgt 50835
 QY 1569 GCTAATTAACCTGAACGACTACGCGACGCAATGCGCAGATGATGATCAGCA 1628
 DB 50836 accgataaacccagcaccagaacatgcagcagtggtatgtgtgtgtgtgtgt 50895
 QY 1629 ATGATGGGTGGGATG 1643
 DB 50896 atggcggtatgtatg 50910

RESULT 9
 ID AAX86152 standard; DNA; 1665 BP.
 AC AAX86152;
 XX 22-SEP-1999 (first entry)
 DE DNA encoding a Streptococcus pneumoniae heat shock protein (Hsp)60-1.
 XX Heat shock protein: Hsp60-1; Immune response; Immunological carrier;
 KM cancer control: tumour; sarcoma; cancer; gene therapy; as.
 XX Streptococcus pneumoniae.
 OS
 XX MO9935270-A1.
 PN 15-JUL-1999.
 PD 29-DEC-1998; 98WO-CA01203.
 PE 31-DEC-1997; 97US-0001737.
 PR (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
 PA Mizzzen L, Wisniewski J;
 PI WPI: 1999-430397/36.
 DR P-PSDB; AAY23301.
 XX New nucleic acid encoding heat shock protein-60 from Streptococcus,
 PT useful in vaccines, as carriers for other immunogens, as anticancer
 agents and for diagnosis
 Claim 3; Fig 1A-B; 176pp; English.

CC The present sequence encodes a heat shock protein, designated Hsp60-1.
 CC The protein, its fragments, variants and fusion proteins, are
 CC used to elicit or enhance an immune response against Streptococcus,
 CC and to elicit a similar response to a target antigen fused to the
 CC protein. Unlike other immunological carriers, Hsp60 proteins are not
 CC immunosuppressive so provide an increased response to any conjugated or
 CC fused antigen. Also, where used for cancer control, they lack the side
 CC effects associated with endotoxins. They can also be used to detect
 CC specific antibodies and in treatment or prevention of tumours
 CC (e.g. sarcoma or cancers of breast, ovary, prostate, lung, pancreas or
 CC liver). The Hsp60 polynucleotide is used for recombinant production
 CC of the protein, as a source of primers and probes for detecting
 CC streptococci in standard hybridization/amplification assays, and
 CC therapeutically in gene therapy vectors.

SO Sequence 1665 BP; 438 A; 401 C; 480 G; 346 T; 0 other;

Query Match 35.6%; Score 590.6; DB 20; Length 1665;
 Best Local Similarity 61.4%; Pred. No. 7.4e-145;
 Matches 1001; Conservative 0; Mismatches 619; Indels 9; Gaps 3;

QY 1 GAATTCGGCTTCATAT---GCAAAAGAAATCAATTTTCAGCAGATGCGGCTGCGCA 57

DB 1 gaattcggcttcataatgctgagcctaaagcctaaatctcgttaacgacgctcgtgtgaaa 60
 QY 58 TGGTGGCGCGAATTTGATATCTTACAGATACCGTCAAGATTAACGCTTGCTTAAAGGCG 117
 DB 61 tgcctgcgcgctaaagctactgctgagatgcagtgaaagctaacctcctgcgcacaaagcgc 120
 QY 118 GCATCTTCTCTTAAAGAAACCTTTGGTTCTTCCCTTAATTAATTAAGACGGGTAAACA 177
 DB 121 gtaacgtactctgataaactcttcggtgacacgcacacacacacacacacacacacac 180
 QY 178 TTGCTAAGAGATCGAATTAAGATCATTTTGAAGACATGAGCAAAATGAGTGTCTG 237
 DB 181 tagcacgtgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaat 240
 QY 238 AAGTGGCTCTTAAAGCAATGATATGCTGCTGATGGGACGACTGCAACGTTTGA 297
 DB 241 aagcttgcctcctaagcgaacgc 300
 QY 298 CACAGCCATTGTTCTATGAAGAGACTTAAATATGACAGACGCTTATTCATTTGTA 357
 DB 301 ctacgtccatcactcactcactcactcactcactcactcactcactcactcactcactcactc 360
 QY 358 TCCGTGAGCGATTGAAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAGCCATTGCTC 417
 DB 361 tgaacggtggtatcgac 420
 QY 418 AACCTGATCTGCGCAGAGAGACTTATGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 474
 DB 421 taccgtgctccgactcctaagcctatcctcctcctcctcctcctcctcctcctcctcctcct 480
 QY 475 AAAAGTTGAGAGATATCTCAGAACTATGAGCTATGAGCTGTGGCAACGATGATGATTA 534
 DB 481 aaacggtgagtaaacctatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 540
 QY 535 CCATGGAAGATTCGAGAGATATGGAAGCAAGAACTTGAAGCTTGAAGCATTAATTTG 594
 DB 541 ccgttgaagagcgtacacggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 600
 QY 595 ACCGTGTTTACCTGCTCAATATGATGATGATGATGATGATGATGATGATGATGATGATG 654
 DB 601 accgtgcttactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 660
 QY 655 AAAACCATTTATCTTAAATCAAGCAATTAAGTCAAAATCTCAAGATTTTCCAC 714
 DB 661 aaagccgttcaatcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 720
 QY 715 TACTTGAGAGATTTCTTAAACCAACCGCTCATTTACTCATTTATTTGATGATGATG 774
 DB 721 tctctgaagcgttagcgaagcagcgaacccgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 780
 QY 775 GGAAGCACTTCAACCGCTGCTGCAACATATCGTGATCTTCAATGATGATGATGATG 834
 DB 781 ggaagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 840
 QY 835 TCAAGCGCAGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 894
 DB 841 ttaagcaccggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 900
 QY 895 CAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 954
 DB 901 ccggtggtacgtatcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 960
 QY 955 CCGTTGAGACGCTGCTTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 1014
 DB 961 atcttgccagcgaagcgaagcgtgtgtatatacaaaagatacacacacacacacacacac 1020
 QY 1015 CAGGAAGTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1074
 DB 1021 tgggtggaagagcgtcgaatccagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1080
 QY 1075 CAATCTTGACTTTGACCGTGAAGAAACCTTAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 1134


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Db 547 ctgcggaggaactcggagctggttgaaagatcagcttcgacgcgctcctccct 606
OY 615 TACATGCTCAGACAGACATGAAAAATGTTGACACCTTGAACCCATTATCTATC 674
Db 607 tctctcattcaaacacgcgaaactcgcagctagaaactgaaagccgcttcctctcg 666
OY 675 ACGATTAATAAAGTGTCAACATCCAGACATTTTGCCTTACTGAGAGATGCTTAAA 734
Db 667 gctgcacagaaataatccacatccgcgaaatcgcgcttcctgaaagcgttcgcaaa 726
OY 735 ACCAACCGCTCTTACTCATTTATGACAGATGATGTGATGGAACCTTCAACCTT 794
Db 727 gcaaggcaaacccgcctgcatcctgcaagatcgtgaagagcgcaagcgtcgtaac 786
OY 795 GTCCTGAACAGATTCGTGCTACTTTCATGCTGCTGCTGCTCAAGCCGAGATTGGT 854
Db 787 gctgttaacacacatcgtgagctcgtgaagagctcgcgtgttaaaagcccggtctgc 846
OY 855 GATCGTCTAAAGCTATGCTTGAAGACATTCGTAATCTGACAGGTGCTACATGATTA 914
Db 847 gacgcgcgaaagcctacgcgcaggaatcgcacccctgcgcgcgtacccgtgactct 906
OY 915 GAGGATCTAGCATGTAATTAAGATGCTACATGACAGCCCTTGAGACAGCTGCTAAG 974
Db 907 gaagagatcgtgtagagctcgtgaagaaagcaaccctggaagacctggtcagcgtaac 966
OY 975 ATTACAGTTGATTAAGATGACAGTAAATGTTGAAAGTCTGAGAAAGTCAAGTATT 1034
Db 967 gctgtgatacaacaagaacacacacatacatalcagcggtggtggaagagcgtgcaac 1026
OY 1035 GCTAACCTGATTCAGCTGATTAATGCAATTAAGAAACAACCTTCTGACTTGAACCT 1094
Db 1027 cagggcgctgtgctcagatccgcagcagatgtaagaaagcaacttcgactacgacct 1086
OY 1095 GAAAAACCTACAAAGACGTTGGGCAATTAAGCTGGGTGCTGCTGCTATCAAAAGTGA 1154
Db 1087 gaaataactcgcggagaaacgctagcgaactcgcgcagcgcgcttcgcatcaaaagtggt 1146
OY 1155 GCTCCACAGACAGACGCTTAAAGAAATGAAAATCGCTGAGATGCTTAAATGCT 1214
Db 1147 gctgtcactcgaagctgtaaatgtaaaagaaagaaagcgcgtgtgaagagccctgcac 1206
OY 1215 ACACGTGACAGCCGTTGAAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1274
Db 1207 accgctgctgcgtgtagaagaaagcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1266
OY 1275 ATTGAAAAAAGTAGACGCTTTGAGCTTGAAGGCGATGCTACTGACGATACAA--TT 1331
Db 1267 ggcgtcaaaactgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1326
OY 1332 GTGCTTCTGCTCTAGAGAGCCTGTACGTCAAAATGCTTAAATGCTGGGTGAGAGGC 1391
Db 1327 gcaacgcgcgtcaatcgtgaagctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1386
OY 1392 TCCGATGATTGACAGTGTGAAAAACACCCCTGCAGAGAACGATTTAATGCTGCAACA 1451
Db 1387 tctgtgtgtctcaacacgcgtttaaagcgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1446
OY 1452 GGTGAGTGGTGTATGATTAAGAGAGAAATCATTTGACCTGTCAAGATCAACGATCA 1511
Db 1447 gaagaatcgcgcaacatcgcacatcgcgtatccgcgtatccaaacaaagtaacgtctct 1506
OY 1512 GGGCTTCAAAATGAGTGTGATGCTTAAATGATGCTTAAATGATGATGCTTAAATG 1571
Db 1507 gctcgcgcgtcgcgaagctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1566
OY 1572 AATTAACCTGAACAGCTACGCCAGCGCAGCAATGCCAGAGATGAG 1620
Db 1567 gacctgcgcaaaaacgatgacgtccttaggcgtcgtgcgcgtatggt 1615

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RESULT 11

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AAC90805
ID AAC90805 standard; DNA; 1647 BP.
AC AAC90805;
XX
DT 16-MAR-2001 (first entry)
XX
DE Escherichia coli GroEL nucleotide sequence SEQ ID NO:2.
KW Escherichia coli; GroEL; mutant; mutelin; improved stability;
KW chaperone; neurotropic; neuroprotective; Alzheimer's disease;
KW prion disease; Creutzfeldt-Jacob's disease; CJD; ds.
OS Escherichia coli.
XX
PN MO200073463-A1.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000MO-GB02019.
XX
PR 27-MAY-1999; 99GB-0012445.
XX
PA (MEDICAL RES COUNCIL.
PI Buckle AM, Fersht A;
XX
DR WPI. 2001-061543/07.
XX
DR P-PSDB; AAB50536.
XX
PT Novel GroEL chaperone polypeptide, its homologue or fragment comprising
PT modifications in specified amino acid residues of GroEL protein
PT sequence, used to treat diseases associated with protein/polypeptide
PT structure.
XX
PS Disclosure: Page 47-49; 58pp; English.
XX
CC The present invention describes a GroEL chaperone polypeptide (CP) (1),
CC its homologue, or fragment having protein refolding activity, and
CC comprising one or more amino acid modifications at any one of amino
CC residues 207, 212, 217, 223, 233, 267, 271, 294, 305, 308 and 326 of the
CC fully defined GroEL protein sequence given in AAB50536, or their
CC equivalent positions in other homologous CPs. (1) can have neurotropic and
CC neuroprotective activity. (1) can be used in therapy (i.e. gene
CC therapy). (1) is used in the manufacture of medicament for treating a
CC disease associated with protein/polypeptide structure. (1) is immediately
CC a solid phase, on contact with a molecule reconditions it, in which the
CC molecule is subjected to inactivation or denaturation prior to contact
CC with (1). The solid phase is a chromatographic matrix and the contact of
CC the molecule and (1) is carried out by applying the molecule to the top
CC of a bed of the matrix packed in a column and then eluting the molecule
CC through the column. (1) is useful for altering the structure of a
CC molecule by folding, unfolding or refolding. Preferably, the
CC stoichiometry between the chaperone (1) and the molecule being altered
CC is about 1:1. (1) is also useful for purifying or increasing the yield,
CC specific activity and/or quality of biological molecules. (1) can also
CC be used for treating a animal or human patient suffering from a disease
CC associated with protein or polypeptide structure. The polypeptides when
CC administered either directly or via nucleic acid constructs may be
CC useful for treating Alzheimer's disease and prion diseases including
CC Creutzfeldt-Jacob's disease. The mutant or modified polypeptides have
CC increased stability while retaining full chaperone activity. The present
CC sequence encodes the Escherichia coli GroEL chaperone, which can be
CC modified for use in the present invention.
XX
SQ Sequence 1647 BP; 437 A; 394 C; 477 G; 339 T; 0 other;

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Query Match 35.5%; Score 589.8; DB 22; Length 1647;
Best Local Similarity 61.3%; Pred. No. 1.2e-144;
Matches 986; Conservative 0; Mismatches 617; Indels 6; Gaps 2;
OY 18 GCATAAGAAATCAATTTTCACGACATGCGCGCTGCTGCCATGCTGGCGGAGATGATG 77

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[illegible]

.....GATTCATTCGCTC 41/

350 360

1381 ccaacgcccggcgaaggccatctgtgtgaccaaacaacgtgaagcagcggaagttaact 1440

Sequence 1635 BP; 448 A; 440 C; 456 G; 291 T; 0 other;

[illegible]

XX WPI: 1999-081217/07.
XX
XX
XX New isolated *Borrelia burgdorferi* nucleic acids - used to develop
PT products for the detection, diagnosis, characterisation, prevention
PT and therapy of infections, particularly Lyme disease
XX
XX
PS Claim 1: Page 157-671, 1128pp: English.
XX
XX
CC AAx20248 to AAx20402 represent polynucleotide sequences isolated from
CC *Borrelia burgdorferi* (Bb). Products derived from Bb can be used for
CC the detection, diagnosis, characterisation, prevention and therapy of
CC Bb infections, e.g. Lyme disease. They can also be used for the
CC production of biosynthetic products, e.g. enzymes. *Borrelia* belongs
CC to a family of motile, spiral-shaped bacteria called spirochetes.
CC Spirochetes are pathogenic in humans and *Borrelia* causes epidemic and
CC endemic relapsing fever, and Lyme borreliosis, more commonly known as
XX Lyme disease.
XX
XX
XX Sequence 910715 BP: 327171 A; 129646 C; 130753 G; 323091 T; 54 other;

Query Match	Best Local Similarity	33.28%	Score 551.6:	DB 20:	Length 910715:
Matches	980:	Conservative	0:	Mismatches 633:	Indels 15:
					Gaps 3
QY 10	TTTCATATGCGCAAAAGAAATCAAAATTTTTCACAGACATCGCGTCTCCATGTGCGCGAG	69			
Db 222236	TTTTATGGCTTAAGACATATATTTTAAATGAGATCTGTGAAAAAGCTTACTTATGTGCGG	222177			
OY 70	TTGATATATGTAGACAGATACCGTCMAAGTAACGTTGGTCCCTTAAGGGCGCAATGGTTC	129			
Db 222176	TTGAAAAATTTATCCAAATGCTGTGTAAGTAACCTTGGCGCAAAAGGAAATATGCTCTTA	222117			
OY 130	TTGAAAAAGCTTTGGTCTCCCTTAATACCTAATAGAGGGGTAAACCATTCGTAAGACA	189			
Db 222116	TTGATTAATAATTTGGCTCTCCCAACGCTTACAAAGATGGGATTAGCGTCTCGTAGA	222057			
OY 190	TCGATTTGGAAGATCAATTTTGAAGATGGAGCAAAATTTGATGTCTGAATGGCTCTTA	249			
Db 222056	TTGACCTTGAAAAATCCGTTTGGAAAAACATGGGGCGACACCTTTTAAAGAAAGTTGCTATTA	221997			
OY 250	AAACCAATGATATTTGCTGTGATGGAGGACACTACGCAACAGTTTGTACACAAGCCATTT	309			
Db 221996	AAACAAATGATGTCTGTGGATGAGAACAAACAGTCAAGTCTTGCTTATGCTATATG	221937			
OY 310	TTTCATGAAGGACTAAAAATATGTCAGCGAGGTCTAATCCATATGGTATCCGTCAGGCA	369			
Db 221936	CAAGGAAGAGCTTAAGAAATATGTCTTTCACAGAAATCAATCTTATGGAAATAAAAAGGGA	221877			
OY 370	TTGAACACGCAACGACACAGCTGTTGAAGCCCTTGAAGCCATTTGCTCAACGCTATCTGA	429			
Db 221876	TGATATCAACGCTGTAAATTTGGCGCTGAGAAAAATTCGTCAGCTCGCAAAAAAGATTACA	221817			
OY 430	GCAAGGAAGCTATTTGCTCAGTGTGCGTCAGATCATCACGCTGTGAAA--AAGTTGGAG	486			
Db 221816	CAAAAGAAGAGATTTGCACAAAGTASCTCAATTTCTGCTAATATATGACGTATATATAGGTG	221757			
OY 487	AGTATATCTAGAGCTATGAGAGCTGTGGCAACATGGTGTGATTTACCATTCGAAGANT	546			
Db 221756	AAAAAATGCTGTGCGCAATGATTAAGTTGGAAGAAAGTGTATTATTAACAGTTGAAGAGT	221697			
OY 547	CTCAGGATATGGAACAGAACTTGAAGGTGTGAAGGATGACATTTGACCGTGTATCC	606			
Db 221696	CAAAAACCTTTGATATCTACGATTTCTTATGTTGAGGGGTATGCAATTTGATAGAGATATC	221637			
OY 607	TGTCCTAATTCATGAGTGCACAGACATTTGAATAAGTTGGTAGACCTGTGAAAACCATTTA	666			
Db 221636	TTTCTCCTTATTTTCTACCAATAAAGAAATATGAGATGTAAATTTTGACGATGGTTTCA	221577			
OY 667	TCCTAATCAACGATAAAAAAGTGTCAACATCCACAGACATTTTGCACACTTGAAGAG	726			
Db 221576	TATTTGATATATGGAAGAAAGATATGCTCTATTAATAAGAGCTTTTATACAGTGTCTTGGAAG	221517			

